

<110> Merck & Co., Inc.

<130> 21490Y PCT

<151> 2004-02-18

<160> 19

<170> FastSEQ for Windows Version 4.0

 $\langle 210 \rangle$ 1

<211> 260

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> truncated derivative of sai-1

 $\langle 400 \rangle$ 1

- 1 -

Val Thr Lys His Asn Glu Thr Pro Lys Gln Ala Ser Lys Ala Lys Glu
 245 250 255
 Leu Pro Lys Thr
 260

<210> 2
 <211> 264
 <212> PRT
 <213> S. aureus

<220>

<400> 2
 Met Gly Thr Gln Val Ser Gln Ala Thr Ser Gln Pro Ile Asn Phe Gln
 1 5 10 15
 Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met Asp Asp Tyr Met
 20 25 30
 Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys Tyr Tyr Phe Gln
 35 40 45
 Ala Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr Lys Phe Tyr Asn
 50 55 60
 Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn Asp Asp Lys Lys
 65 70 75 80
 Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro Gly Tyr Lys Ser
 85 90 95
 Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile Asn Tyr Asn His
 100 105 110
 Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile Pro Thr Leu Ala
 115 120 125
 Asp Ala Ala Lys Pro Asn Asn Val Lys Pro Val Gln Pro Lys Pro Ala
 130 135 140
 Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro Val Gln Pro Lys Val
 145 150 155 160
 Glu Lys Val Lys Pro Ala Val Thr Ala Pro Ser Lys Asn Glu Asn Arg
 165 170 175
 Gln Thr Thr Lys Val Val Ser Ser Glu Ala Thr Lys Asp Gln Ser Gln
 180 185 190
 Thr Gln Ser Ala Arg Thr Val Lys Thr Thr Gln Thr Ala Gln Asp Gln
 195 200 205
 Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala Thr Ala Lys Ser Glu
 210 215 220
 Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln Gln Thr Asn Lys
 225 230 235 240
 Val Thr Lys Gln Asn Glu Val His Lys Gln Gly Pro Ser Lys Asp Ser
 245 250 255
 Lys Ala Lys Glu Leu Pro Lys Thr
 260

<210> 3
 <211> 280
 <212> PRT
 <213> Artificial Sequence

<220>

<223> amino His-tagged construct of SEQ ID NO: 1

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<400> 3
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1          5          10          15
Arg Gly Ser His Met Gly Thr Gln Val Ser Gln Ala Thr Ser Gln Pro
      20          25          30
Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met
      35          40          45
Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys
      50          55          60
Tyr Tyr Phe Gln Thr Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr
65          70          75          80
Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn
      85          90          95
Asp Asn Lys Lys Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro
      100          105          110
Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile
      115          120          125
Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile
      130          135          140
Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val Lys Pro Val Gln
145          150          155          160
Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro Val
      165          170          175
Gln Pro Lys Val Glu Lys Val Lys Pro Thr Val Thr Thr Thr Ser Lys
      180          185          190
Val Glu Asp Asn His Ser Thr Lys Val Val Ser Thr Asp Thr Thr Lys
      195          200          205
Asp Gln Thr Lys Thr Gln Thr Ala His Thr Val Lys Thr Ala Gln Thr
      210          215          220
Ala Gln Glu Gln Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala Thr
225          230          235          240
Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln
      245          250          255
Gln Thr Asn Lys Val Thr Lys His Asn Glu Thr Pro Lys Gln Ala Ser
      260          265          270
Lys Ala Lys Glu Leu Pro Lys Thr
      275          280

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<210> 4
<211> 284
<212> PRT
<213> Artificial Sequence

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<220>
<223> amino His-tagged construct of SEQ ID NO: 2

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<400> 4
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1          5          10          15
Arg Gly Ser His Met Gly Thr Gln Val Ser Gln Ala Thr Ser Gln Pro
      20          25          30
Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met
      35          40          45

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Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys
 50      55      60
Tyr Tyr Phe Gln Ala Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr
65      70      75      80
Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn
      85      90      95
Asp Asp Lys Lys Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro
      100      105      110
Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile
      115      120      125
Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile
      130      135      140
Pro Thr Leu Ala Asp Ala Lys Pro Asn Asn Val Lys Pro Val Gln
145      150      155      160
Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro Val
      165      170      175
Gln Pro Lys Val Glu Lys Val Lys Pro Ala Val Thr Ala Pro Ser Lys
      180      185      190
Asn Glu Asn Arg Gln Thr Thr Lys Val Val Ser Ser Glu Ala Thr Lys
      195      200      205
Asp Gln Ser Gln Thr Gln Ser Ala Arg Thr Val Lys Thr Thr Gln Thr
      210      215      220
Ala Gln Asp Gln Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala Thr
225      230      235      240
Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln
      245      250      255
Gln Thr Asn Lys Val Thr Lys Gln Asn Glu Val His Lys Gln Gly Pro
      260      265      270
Ser Lys Asp Ser Lys Ala Lys Glu Leu Pro Lys Thr
      275      280

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<210> 5

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> carboxyl His-tagged construct of SEQ ID NO: 1

<400> 5

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Met Gly Thr Gln Val Ser Gln Ala Thr Ser Gln Pro Ile Asn Phe Gln
 1      5      10      15
Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met Asp Asp Tyr Met
      20      25      30
Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys Tyr Tyr Phe Gln
      35      40      45
Thr Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr Lys Phe Tyr Asn
      50      55      60
Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn Asp Asn Lys Lys
65      70      75      80
Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro Gly Tyr Lys Ser
      85      90      95
Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile Asn Tyr Asn His
      100      105      110

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Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile Pro Thr Leu Ala
      115      120      125
Asp Ala Ala Lys Pro Asn Asn Val Lys Pro Val Gln Pro Lys Pro Ala
      130      135      140
Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro Val Gln Pro Lys Val
145      150      155      160
Glu Lys Val Lys Pro Thr Val Thr Thr Thr Ser Lys Val Glu Asp Asn
      165      170      175
His Ser Thr Lys Val Val Ser Thr Asp Thr Thr Lys Asp Gln Thr Lys
      180      185      190
Thr Gln Thr Ala His Thr Val Lys Thr Ala Gln Thr Ala Gln Glu Gln
      195      200      205
Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala Thr Ala Lys Ser Glu
      210      215      220
Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln Gln Thr Asn Lys
225      230      235      240
Val Thr Lys His Asn Glu Thr Pro Lys Gln Ala Ser Lys Ala Lys Glu
      245      250      255
Leu Pro Lys Thr Leu Glu His His His His His His
      260      265

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<210> 6
 <211> 395
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino His-tagged construct of SEQ ID NO: 7

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<400> 6
Met His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
 1      5      10      15
Gly Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp
      20      25      30
Ser Pro Asp Leu Gly Thr Asp Asp Asp Asp Lys Ala Met Gly Thr Lys
      35      40      45
His Tyr Leu Asn Ser Lys Tyr Gln Ser Glu Gln Arg Ser Ser Ala Met
      50      55      60
Lys Lys Ile Thr Met Gly Thr Ala Ser Ile Ile Leu Gly Ser Leu Val
65      70      75      80
Tyr Ile Gly Ala Asp Ser Gln Gln Val Asn Ala Ala Thr Glu Ala Thr
      85      90      95
Asn Ala Thr Asn Asn Gln Ser Thr Gln Val Ser Gln Ala Thr Ser Gln
      100      105      110
Pro Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His
      115      120      125
Met Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn
      130      135      140
Lys Tyr Tyr Phe Gln Thr Val Leu Asn Asn Ala Ser Phe Trp Lys Glu
145      150      155      160
Tyr Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val
      165      170      175
Asn Asp Asn Lys Lys Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu
      180      185      190

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Pro Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val Val Pro Gln
 195 200 205
 Ile Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala
 210 215 220
 Ile Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val Lys Pro Val
 225 230 235 240
 Gln Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro
 245 250 255
 Val Gln Pro Lys Val Glu Lys Val Lys Pro Thr Val Thr Thr Thr Ser
 260 265 270
 Lys Val Glu Asp Asn His Ser Thr Lys Val Val Ser Thr Asp Thr Thr
 275 280 285
 Lys Asp Gln Thr Lys Thr Gln Thr Ala His Thr Val Lys Thr Ala Gln
 290 295 300
 Thr Ala Gln Glu Gln Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala
 305 310 315 320
 Thr Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser
 325 330 335
 Gln Gln Thr Asn Lys Val Thr Lys His Asn Glu Thr Pro Lys Gln Ala
 340 345 350
 Ser Lys Ala Lys Glu Leu Pro Lys Thr Gly Leu Thr Ser Val Asp Asn
 355 360 365
 Phe Ile Ser Thr Val Ala Phe Ala Thr Leu Ala Leu Leu Gly Ser Leu
 370 375 380
 Ser Leu Leu Leu Phe Lys Arg Lys Glu Ser Lys
 385 390 395

<210> 7
 <211> 350
 <212> PRT
 <213> S. aureus

<400> 7
 Met Thr Lys His Tyr Leu Asn Ser Lys Tyr Gln Ser Glu Gln Arg Ser
 1 5 10 15
 Ser Ala Met Lys Lys Ile Thr Met Gly Thr Ala Ser Ile Ile Leu Gly
 20 25 30
 Ser Leu Val Tyr Ile Gly Ala Asp Ser Gln Gln Val Asn Ala Ala Thr
 35 40 45
 Glu Ala Thr Asn Ala Thr Asn Asn Gln Ser Thr Gln Val Ser Gln Ala
 50 55 60
 Thr Ser Gln Pro Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu
 65 70 75 80
 Lys Ser His Met Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys
 85 90 95
 Gln Asn Asn Lys Tyr Tyr Phe Gln Thr Val Leu Asn Asn Ala Ser Phe
 100 105 110
 Trp Lys Glu Tyr Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr
 115 120 125
 Thr Val Val Asn Asp Asn Lys Lys Ala Asp Thr Arg Thr Ile Asn Val
 130 135 140
 Ala Val Glu Pro Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val
 145 150 155 160
 Val Pro Gln Ile Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe
 165 170 175

Glu Lys Ala Ile Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val
 180 185 190
 Lys Pro Val Gln Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln
 195 200 205
 Thr Lys Pro Val Gln Pro Lys Val Glu Lys Val Lys Pro Thr Val Thr
 210 215 220
 Thr Thr Ser Lys Val Glu Asp Asn His Ser Thr Lys Val Val Ser Thr
 225 230 235 240
 Asp Thr Thr Lys Asp Gln Thr Lys Thr Gln Thr Ala His Thr Val Lys
 245 250 255
 Thr Ala Gln Thr Ala Gln Glu Gln Asn Lys Val Gln Thr Pro Val Lys
 260 265 270
 Asp Val Ala Thr Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp
 275 280 285
 Asn Lys Ser Gln Gln Thr Asn Lys Val Thr Lys His Asn Glu Thr Pro
 290 295 300
 Lys Gln Ala Ser Lys Ala Lys Glu Leu Pro Lys Thr Gly Leu Thr Ser
 305 310 315 320
 Val Asp Asn Phe Ile Ser Thr Val Ala Phe Ala Thr Leu Ala Leu Leu
 325 330 335
 Gly Ser Leu Ser Leu Leu Leu Phe Lys Arg Lys Glu Ser Lys
 340 345 350

<210> 8
 <211> 354
 <212> PRT
 <213> S. aureus

<400> 8
 Met Thr Lys His Tyr Leu Asn Ser Lys Tyr Gln Ser Glu Gln Arg Ser
 1 5 10 15
 Ser Ala Met Lys Lys Ile Thr Met Gly Thr Ala Ser Ile Ile Leu Gly
 20 25 30
 Ser Leu Val Tyr Ile Gly Ala Asp Ser Gln Gln Val Asn Ala Ala Thr
 35 40 45
 Glu Ala Thr Asn Ala Thr Asn Asn Gln Ser Thr Gln Val Ser Gln Ala
 50 55 60
 Thr Ser Gln Pro Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu
 65 70 75 80
 Lys Ser His Met Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys
 85 90 95
 Gln Asn Asn Lys Tyr Tyr Phe Gln Ala Val Leu Asn Asn Ala Ser Phe
 100 105 110
 Trp Lys Glu Tyr Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr
 115 120 125
 Thr Val Val Asn Asp Asp Lys Lys Ala Asp Thr Arg Thr Ile Asn Val
 130 135 140
 Ala Val Glu Pro Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val
 145 150 155 160
 Val Pro Gln Ile Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe
 165 170 175
 Glu Lys Ala Ile Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val
 180 185 190
 Lys Pro Val Gln Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln
 195 200 205

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Thr Lys Pro Val Gln Pro Lys Val Glu Lys Val Lys Pro Ala Val Thr
210                215                220
Ala Pro Ser Lys Asn Glu Asn Arg Gln Thr Thr Lys Val Val Ser Ser
225                230                235                240
Glu Ala Thr Lys Asp Gln Ser Gln Thr Gln Ser Ala Arg Thr Val Lys
                245                250                255
Thr Thr Gln Thr Ala Gln Asp Gln Asn Lys Val Gln Thr Pro Val Lys
                260                265                270
Asp Val Ala Thr Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp
                275                280                285
Asn Lys Ser Gln Gln Thr Asn Lys Val Thr Lys Gln Asn Glu Val His
290                295                300
Lys Gln Gly Pro Ser Lys Asp Ser Lys Ala Lys Glu Leu Pro Lys Thr
305                310                315                320
Gly Leu Thr Ser Val Asp Asn Phe Ile Ser Thr Val Ala Phe Ala Thr
                325                330                335
Leu Ala Leu Leu Gly Ser Leu Ser Leu Leu Leu Phe Lys Arg Lys Glu
                340                345                350
Ser Lys

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<210> 9

<211> 358

<212> PRT

<213> Artificial Sequence

<220>

<223> carboxyl His-tagged construct of SEQ ID NO: 7

<400> 9

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Met Thr Lys His Tyr Leu Asn Ser Lys Tyr Gln Ser Glu Gln Arg Ser
1                5                10                15
Ser Ala Met Lys Lys Ile Thr Met Gly Thr Ala Ser Ile Ile Leu Gly
                20                25                30
Ser Leu Val Tyr Ile Gly Ala Asp Ser Gln Gln Val Asn Ala Ala Thr
                35                40                45
Glu Ala Thr Asn Ala Thr Asn Asn Gln Ser Thr Gln Val Ser Gln Ala
50                55                60
Thr Ser Gln Pro Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu
65                70                75                80
Lys Ser His Met Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys
                85                90                95
Gln Asn Asn Lys Tyr Tyr Phe Gln Thr Val Leu Asn Asn Ala Ser Phe
                100                105                110
Trp Lys Glu Tyr Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr
                115                120                125
Thr Val Val Asn Asp Asn Lys Lys Ala Asp Thr Arg Thr Ile Asn Val
130                135                140
Ala Val Glu Pro Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val
145                150                155                160
Val Pro Gln Ile Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe
                165                170                175
Glu Lys Ala Ile Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val
                180                185                190

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Lys Pro Val Gln Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln
 195 200 205
 Thr Lys Pro Val Gln Pro Lys Val Glu Lys Val Lys Pro Thr Val Thr
 210 215 220
 Thr Thr Ser Lys Val Glu Asp Asn His Ser Thr Lys Val Val Ser Thr
 225 230 235 240
 Asp Thr Thr Lys Asp Gln Thr Lys Thr Gln Thr Ala His Thr Val Lys
 245 250 255
 Thr Ala Gln Thr Ala Gln Glu Gln Asn Lys Val Gln Thr Pro Val Lys
 260 265 270
 Asp Val Ala Thr Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp
 275 280 285
 Asn Lys Ser Gln Gln Thr Asn Lys Val Thr Lys His Asn Glu Thr Pro
 290 295 300
 Lys Gln Ala Ser Lys Ala Lys Glu Leu Pro Lys Thr Gly Leu Thr Ser
 305 310 315 320
 Val Asp Asn Phe Ile Ser Thr Val Ala Phe Ala Thr Leu Ala Leu Leu
 325 330 335
 Gly Ser Leu Ser Leu Leu Leu Phe Lys Arg Lys Glu Ser Lys Leu Glu
 340 345 350
 His His His His His
 355

<210> 10
 <211> 843
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleic acid sequence encoding SEQ ID NO: 3

<400> 10
 atgggagcagca gccatcatca tcatcatcac agcagcggcc tgggtgccgag cggcagccat 60
 atgggacacac aagttttctca agcaacatca caaccaatta atttccaagt gcaaaaagat 120
 ggctcttcag agaagtcaca catggatgac tatatgcaac accctggtaa agtaattaaa 180
 caaaataata aatattattt ccaaaccgtg ttaaacaatg catcattctg gaaagaatac 240
 aaatttttaca atgcaaacaa tcaagaatta gcaacaactg ttgttaacga taataaaaaa 300
 gcggatacta gaacaatcaa tgttgagctt gaacctggat ataagagctt aactactaaa 360
 gtacatatgt tcgtgccaca aattaattac aatcatagat atactacgca ttgtgaattt 420
 gaaaaagcaa ttcctacatt agctgacgca gcaaaaccaa acaatgttaa accggttcaa 480
 ccaaaaccag ctcaacctaa aacacctact gagcaacta aaccagttca acctaaagtt 540
 gaaaaagtta aacctactgt aactacaaca agcaaagttg aagacaatca ctctactaaa 600
 gttgtaagta ctgacacaac aaaagatcaa actaaaacac aaactgctca tacagttaaa 660
 acagcacaaa ctgctcaaga acaaaataaa gttcaaacac ctgttaaaga tgttgcaaca 720
 gcgaaatctg aaagcaacaa tcaagctgta agtgataata aatcacaaca aactaacaaa 780
 gttacaaaac ataacgaaac gcctaaacaa gcatctaaag ctaaagaatt accaaaaact 840
 tga 843

<210> 11
 <211> 855
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleic acid sequence encoding SEQ ID NO: 4

<400> 11
 atgggcagca gccatcatca tcatcatcac agcagcggcc tggtgccgcg cggcagccat 60
 atgggcacac aagtttctca agcaacatca caaccaatta atttccaagt gcaaaaagat 120
 ggctcttcag agaagtcaca catggatgac tatatgcaac accctggtaa agtgattaaa 180
 caaaataata aatattattht ccaagctgta ttgaacaacg catcattctg gaaagaatac 240
 aaattttaca atgcaaacaa tcaagaatta gcaacaactg ttgttaacga tgataaaaaa 300
 gctgacacta gaacaatcaa tgttgctgtt gaacctgggt ataagagttt aactacaaaa 360
 gtacatatthg tcgtgccaca aattaattat aatcatagat atactacgca tttagaattht 420
 gaaaaagcaa ttcctacatt agctgacgca gcaaaaccaa acaatgttaa accggttcaa 480
 ccaaaacctg ctcaacctaa aacacctact gagcaaacga aaccagttca acctaaagtt 540
 gaaaaagtta aacctgctgt aactgcacca agcaaaaatg aaaacagaca aactacaaaa 600
 gttgtaagta gtgaagctac aaaagatcaa agtcaaacac aaagtgtctg tacagtgaag 660
 acaacacaaa cagctcaaga tcaaaataaa gttcaaacac ctgttaaaga tgttgcaaca 720
 gcgaaatctg aaagcaacaa tcaagctgta agtgacaata aatcacacaa aactaacaaa 780
 gttacaaaaac aaaacgaagt tcataaacia ggaccttcaa aagattctaa agctaaagaa 840
 ttacacaaaaa ctthg 855

<210> 12

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 12

gagatatacc atgggcacaa aacattattht aaacagt 37

<210> 13

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 13

ccggcggccc tcgagtttag attcttttct tttgaa 36

<210> 14

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 14

gagatatacc atgggcacaa aacattattht aaacagt 37

<210> 15

<211> 39

<212> DNA

<213> Artificial Sequence

<220>
<223> primer

<400> 15
ccggcgggccc tcgagttatt tagattcttt tcttttgaa 39

<210> 16
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 16
gagatatacc atgggcacac aagtttctca agcaacatca c 41

<210> 17
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 17
ggtggtgctc gagagttttt ggtaattctt tagctt 36

<210> 18
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 18
gagatatcat atgggcacac aagtttctca agcaacatca c 41

<210> 19
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 19
ggtggtgctc gagtcaagtt tttggtaatt ctttagctt 39